RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _/O/537, 897._

Source: _____ PcT/10

Date Processed by STIC: _____ 6/16/05

ENTERED

RAW SEQUENCE LISTING   DATE: 06/16/2005
PATENT APPLICATION: US/10/537,897   TIME: 10:21:25

        Input Set : A:\pto.da.txt
        Output Set: N:\CRF4\06162005\J537897.raw

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     5 <110> APPLICANT: CropDesign N.V.
     9 <120> TITLE OF INVENTION: Plants having modified growth characteristics and a method
for making the
    10         same
    14 <130> FILE REFERENCE: CD-070-PCT
C--> 18 <140> CURRENT APPLICATION NUMBER: US/10/537,897
C--> 18 <141> CURRENT FILING DATE: 2005-06-07
    18 <160> NUMBER OF SEQ ID NOS: 50
    22 <170> SOFTWARE: PatentIn version 3.1
    26 <210> SEQ ID NO: 1
    28 <211> LENGTH: 692
    30 <212> TYPE: DNA
    32 <213> ORGANISM: Arabidopsis thaliana
    36 <400> SEQUENCE: 1
    37 aatggcgctc gaggctctta catcaccaag attagcttct ccgattcctc ctttgttcga      60
    39 agattcttca gtcttccatg gagtcgagca ctggacaaag ggtaagcgat ctaagagatc     120
    41 aagatccgat ttccaccacc aaaacctcac tgaggaagag tatctagctt tttgcctcat     180
    43 gcttctcgct cgcgacaacc gtcagcctcc tcctcctccg gcggtggaga agttgagcta     240
    45 caagtgtagc gtctgcgaca agacgttctc ttcttaccaa gctctcggtg gtcacaaggc     300
    47 aagccaccgt aagaacttat cacagactct ctccggcgga ggagatgatc attcaacctc     360
    49 gtcggcgaca accacatccg ccgtgactac tggaagtggg aaatcacacg tttgcaccat     420
    51 ctgtaacaag tcttttcctt ccggtcaagc tctcggcgga cacaagcggt gccactacga     480
    53 aggaaacaac aacatcaaca ctagtagcgt gtccaactcc gaaggtgcgg ggtccactag     540
    55 ccacgttagc agtagccacc gtgggtttga cctcaacatc cctccgatcc ctgaattctc     600
    57 gatggtcaac ggagacgacg aagtcatgag ccctatgccg gcgaagaagc ctcggtttga     660
    59 ctttccggtc aaacttcaac tttaaggaaa tt                                    692
    62 <210> SEQ ID NO: 2
    64 <211> LENGTH: 227
    66 <212> TYPE: PRT
    68 <213> ORGANISM: Arabidopsis thaliana
    72 <400> SEQUENCE: 2
    74 Met Ala Leu Glu Ala Leu Thr Ser Pro Arg Leu Ala Ser Pro Ile Pro
    75 1               5                   10                  15
    78 Pro Leu Phe Glu Asp Ser Ser Val Phe His Gly Val Glu His Trp Thr
    79             20                  25                  30
    82 Lys Gly Lys Arg Ser Lys Arg Ser Arg Ser Asp Phe His His Gln Asn
    83         35                  40                  45
    86 Leu Thr Glu Glu Glu Tyr Leu Ala Phe Cys Leu Met Leu Leu Ala Arg
    87     50                  55                  60
    90 Asp Asn Arg Gln Pro Pro Pro Pro Ala Val Glu Lys Leu Ser Tyr
    91 65                  70                  75                  80
    94 Lys Cys Ser Val Cys Asp Lys Thr Phe Ser Ser Tyr Gln Ala Leu Gly
    95             85                  90                  95
    98 Gly His Lys Ala Ser His Arg Lys Asn Leu Ser Gln Thr Leu Ser Gly
```

```
99              100                105                110
102 Gly Gly Asp Asp His Ser Thr Ser Ser Ala Thr Thr Thr Ser Ala Val
103         115                120                125
106 Thr Thr Gly Ser Gly Lys Ser His Val Cys Thr Ile Cys Asn Lys Ser
107     130                135                140
110 Phe Pro Ser Gly Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Glu
111 145                150                155                160
114 Gly Asn Asn Asn Ile Asn Thr Ser Ser Val Ser Asn Ser Glu Gly Ala
115                165                170                175
118 Gly Ser Thr Ser His Val Ser Ser Ser His Arg Gly Phe Asp Leu Asn
119         180                185                190
122 Ile Pro Pro Ile Pro Glu Phe Ser Met Val Asn Gly Asp Asp Glu Val
123         195                200                205
126 Met Ser Pro Met Pro Ala Lys Lys Pro Arg Phe Asp Phe Pro Val Lys
127     210                215                220
130 Leu Gln Leu
131 225
134 <210> SEQ ID NO: 3
136 <211> LENGTH: 50
138 <212> TYPE: DNA
140 <213> ORGANISM: Artificial sequence
144 <220> FEATURE:
146 <223> OTHER INFORMATION: primer PRM3204
148 <400> SEQUENCE: 3
149 ggggacaagt ttgtacaaaa aagcaggctt cacaatggcg ctcgaggctc          50
152 <210> SEQ ID NO: 4
154 <211> LENGTH: 53
156 <212> TYPE: DNA
158 <213> ORGANISM: Artificial sequence
162 <220> FEATURE:
164 <223> OTHER INFORMATION: primer PRM3205
166 <400> SEQUENCE: 4
167 ggggaccact ttgtacaaga aagctgggta atttccttaa agttgaagtt tga      53
170 <210> SEQ ID NO: 5
172 <211> LENGTH: 6
174 <212> TYPE: PRT
176 <213> ORGANISM: Artificial sequence
180 <220> FEATURE:
182 <223> OTHER INFORMATION: QALGGH motif
184 <400> SEQUENCE: 5
186 Gln Ala Leu Gly Gly His
187 1               5
190 <210> SEQ ID NO: 6
192 <211> LENGTH: 6
194 <212> TYPE: PRT
196 <213> ORGANISM: Artificial sequence
200 <220> FEATURE:
202 <223> OTHER INFORMATION: NNM box
204 <220> FEATURE:
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       206 <221> NAME/KEY: MISC_FEATURE
       208 <222> LOCATION: (3)..(3)
       210 <223> OTHER INFORMATION: Xaa can be either methionine or tryptophan
       214 <400> SEQUENCE: 6
W-->   216 Asn Asn Xaa Gln Met His
       217 1               5
       220 <210> SEQ ID NO: 7
       222 <211> LENGTH: 7
       224 <212> TYPE: PRT
       226 <213> ORGANISM: Artificial sequence
       230 <220> FEATURE:
       232 <223> OTHER INFORMATION: EAR motif
       234 <220> FEATURE:
       236 <221> NAME/KEY: MISC_FEATURE
       238 <222> LOCATION: (1)..(1)
       240 <223> OTHER INFORMATION: Xaa can be any hydrophobic amino acid (Ala, Cys, Phe, Gly,
His, I
       241       le, Lys, Leu, Met, Arg, Thr, Val, Trp or Tyr)
       245 <220> FEATURE:
       247 <221> NAME/KEY: MISC_FEATURE
       249 <222> LOCATION: (5)..(5)
       251 <223> OTHER INFORMATION: Xaa can be any hydrophobic amino acid (Ala, Cys, Phe, Gly,
His, I
       252       le, Lys, Leu, Met, Arg, Thr, Val, Trp or Tyr)
       256 <220> FEATURE:
       258 <221> NAME/KEY: MISC_FEATURE
       260 <222> LOCATION: (6)..(6)
       262 <223> OTHER INFORMATION: Xaa can be any amino acid or no amino acid
       266 <400> SEQUENCE: 7
W-->   268 Xaa Asp Leu Asn Xaa Xaa Pro
       269 1               5
       272 <210> SEQ ID NO: 8
       274 <211> LENGTH: 7
       276 <212> TYPE: PRT
       278 <213> ORGANISM: Artificial sequence
       282 <220> FEATURE:
       284 <223> OTHER INFORMATION: B-Box
       286 <220> FEATURE:
       288 <221> NAME/KEY: MISC_FEATURE
       290 <222> LOCATION: (3)..(3)
       292 <223> OTHER INFORMATION: Ser can be serine or no amino acid
       296 <220> FEATURE:
       298 <221> NAME/KEY: MISC_FEATURE
       300 <222> LOCATION: (6)..(6)
       302 <223> OTHER INFORMATION: Xaa can be any amino acid
       306 <400> SEQUENCE: 8
W-->   308 Lys Arg Ser Lys Arg Xaa Arg
       309 1               5
       312 <210> SEQ ID NO: 9
       314 <211> LENGTH: 12
       316 <212> TYPE: PRT
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Input Set : A:\pto.da.txt
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318 <213> ORGANISM: Artificial sequence
322 <220> FEATURE:
324 <223> OTHER INFORMATION: L-Box
326 <220> FEATURE:
328 <221> NAME/KEY: MISC_FEATURE
330 <222> LOCATION: (2)..(2)
332 <223> OTHER INFORMATION: Xaa can be any amino acid
336 <220> FEATURE:
338 <221> NAME/KEY: MISC_FEATURE
340 <222> LOCATION: (4)..(5)
342 <223> OTHER INFORMATION: Xaa can be any amino acid
346 <220> FEATURE:
348 <221> NAME/KEY: MISC_FEATURE
350 <222> LOCATION: (7)..(7)
352 <223> OTHER INFORMATION: Xaa can be any amino acid
356 <220> FEATURE:
358 <221> NAME/KEY: MISC_FEATURE
360 <222> LOCATION: (10)..(11)
362 <223> OTHER INFORMATION: Xaa can be any amino acid
366 <400> SEQUENCE: 9
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369 1               5                  10
372 <210> SEQ ID NO: 10
374 <211> LENGTH: 1006
376 <212> TYPE: DNA
378 <213> ORGANISM: Datisca glomerata
382 <400> SEQUENCE: 10
383 ggcacgagga caaattctct ctctatcctc tgaatatctt tggtttgtga actgagaagc    60
385 tattagatgg ctctagaagc gctcaactct ccgaccacag ctacgccggt gtttcactac   120
387 gacgacccca gcttgaatta ccttgagcca tggaccaagc gtaagcgttc caagcgtacg   180
389 cgcttagata gcccccatacc gaggaagagt accttgcttt ctgcctcatc atgctcgctc   240
391 gtggccgcgt tgcctctgca aatcgacggg attctcagtc ttccattcag attcagcctg   300
393 aagcaacgac ttcggctacc aaagtcagtt ataagtgctc tgtgtgcgat aaggcctttt   360
395 cgtcttatca ggctttgggt gggcacaagg ccagccacag aaagctcgct ggcggcgaag   420
397 atcaatcgac ttcctttgcc accacgaatt cagccaccgt cactaccacc acagcctccg   480
399 gaggtggtgg caggtctcat gagtgttcta tttgccacaa atcgttcccg actggccagg   540
401 ccttgggtgg tcacaagcgc tgccactacg aaggcagtat cggcggcaat agtattcacc   600
403 accacaacaa taccaccaac agcggaagca acggtggcat gagcatgacc tccgaagtag   660
405 gttccacaca cacagtcagc cacagtcacc gtgacttcga tctcaacatc ccggccttgc   720
407 cggagtttcg gtcgaatttc ttcatatccg gggatgacga ggtcgagagt cctcatccgg   780
409 ccaagaaacc ccgtatattg atgaaataaa acatttctca agatcactga accaggcttt   840
411 agtttcttta taggaggaga tttaaaaaag tagtatctct ctttctttat ccgtaggata   900
413 attaatatat ttcgtgtaca taaatttgta gttctttaac acactctgtt tcattttctt   960
415 gctttgctca actttgtatt ggttatttca ttatgaaaat tcaatt              1006
418 <210> SEQ ID NO: 11
420 <211> LENGTH: 247
422 <212> TYPE: PRT
424 <213> ORGANISM: Datisca glomerata
428 <400> SEQUENCE: 11
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RAW SEQUENCE LISTING   DATE: 06/16/2005
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430 Met Ala Leu Glu Ala Leu Asn Ser Pro Thr Thr Ala Thr Pro Val Phe
431 1                   5                  10                  15
434 His Tyr Asp Asp Pro Ser Leu Asn Tyr Leu Glu Pro Trp Thr Lys Arg
435             20                  25                  30
438 Lys Arg Ser Lys Arg Thr Arg Leu Asp Ser Pro His Thr Glu Glu Glu
439         35                  40                  45
442 Tyr Leu Ala Phe Cys Leu Ile Met Leu Ala Arg Gly Arg Val Ala Ser
443     50                  55                  60
446 Ala Asn Arg Arg Asp Ser Gln Ser Ser Ile Gln Ile Gln Pro Glu Ala
447 65                  70                  75                  80
450 Thr Thr Ser Ala Thr Lys Val Ser Tyr Lys Cys Ser Val Cys Asp Lys
451             85                  90                  95
454 Ala Phe Ser Ser Tyr Gln Ala Leu Gly Gly His Lys Ala Ser His Arg
455             100                 105                 110
458 Lys Leu Ala Gly Gly Glu Asp Gln Ser Thr Ser Phe Ala Thr Thr Asn
459         115                 120                 125
462 Ser Ala Thr Val Thr Thr Thr Thr Ala Ser Gly Gly Gly Gly Arg Ser
463     130                 135                 140
466 His Glu Cys Ser Ile Cys His Lys Ser Phe Pro Thr Gly Gln Ala Leu
467 145                 150                 155                 160
470 Gly Gly His Lys Arg Cys His Tyr Glu Gly Ser Ile Gly Gly Asn Ser
471             165                 170                 175
474 Ile His His His Asn Asn Thr Thr Asn Ser Gly Ser Asn Gly Gly Met
475             180                 185                 190
478 Ser Met Thr Ser Glu Val Gly Ser Thr His Thr Val Ser His Ser His
479         195                 200                 205
482 Arg Asp Phe Asp Leu Asn Ile Pro Ala Leu Pro Glu Phe Arg Ser Asn
483     210                 215                 220
486 Phe Phe Ile Ser Gly Asp Asp Glu Val Glu Ser Pro His Pro Ala Lys
487 225                 230                 235                 240
490 Lys Pro Arg Ile Leu Met Lys
491                 245
494 <210> SEQ ID NO: 12
496 <211> LENGTH: 996
498 <212> TYPE: DNA
500 <213> ORGANISM: Glycine max
504 <400> SEQUENCE: 12
505 aaaattctca ctctctctct catctcgaga tcatagtatc atattcaata tcatttcata        60
507 ccaaacacat ggctttggaa gctctcaact caccaacaac aaccgctcca tcttttccct       120
509 ttgacgaccc aactattcca tgggcgaaac gaaaacgttc aaagcgttct cgcgaccatc       180
511 cttctgaaga agagtacctc gccctctgcc tcatcatgct cgctcgcggc ggcaccacca       240
513 ccgtcaacaa ccgccacgtc agccctccgc cgctacagcc acagccacag ccgacaccag       300
515 atccttccac caagctcagt tacaaatgct ccgtttgcga caagagcttc ccctcttacc       360
517 aagcgctcgg tggacacaag gccagtcacc ggaaactcgc cggcgccgcc gaagaccaac       420
519 cccccagcac caccacttcc tccgccgccg ccaccagctc cgcctccgga ggtaaggccc       480
521 atgagtgctc catttgccac aaatccttcc ccaccggaca ggcccttggc ggacacaaac       540
523 gttgtcacta cgaaggtaac ggtaacggaa ataacaacaa cagtaacagc gttgtcaccg       600
525 tcgcctcgga aggcgtgggc tccacccaca ctgtcagtca cggccaccac cgcgacttcg       660
527 atctcaacat cccggccttt ccggattttt cgaccaaggt cggagaagac gaggttgaga       720
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 06/16/2005
PATENT APPLICATION: US/10/537,897   TIME: 10:21:26

Input Set : **A:\pto.da.txt**
Output Set: **N:\CRF4\06162005\J537897.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; Xaa Pos. 3
Seq#:7; Xaa Pos. 1,5,6
Seq#:8; Xaa Pos. 6
Seq#:9; Xaa Pos. 2,4,5,7,10,11
Seq#:40; N Pos. 406,581,582,589

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 9

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/537,897

DATE: 06/16/2005
TIME: 10:21:26

Input Set : **A:\pto.da.txt**
Output Set: **N:\CRF4\06162005\J537897.raw**

```
L:18 M:270 C: Current Application Number differs, Replaced Current Application No
L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:216 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:2221 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:360
M:341 Repeated in SeqNo=40
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